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SUBSTITUTE SEQUENCE LISTING

<110> Vannuffel, Pascal
Gala, Jean-Luc

<120> GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES
FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS

<130> VANM145.001APC

<140> 09/509,234

<141> 1998-09-28

<160> 64

<170> PatentIn version 3.0

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<212> DNA

<213> Staphylococcus femA Consensus Sequence

<220>

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nnannnnnnn	ganncncann	tagtngnat	naanaanaan	nataangang	tnattgcngc	180
ntgnntnnntn	acngcngtnc	cngtnatgaa	antntnaan	tantttatt	cnaannnggg	240
nccngtnatn	gatttnana	annnaganct	ngtncantnn	ttctttaang	anttnnnnaa	300
ntattnnaaa	nannannntn	nnntatannt	nnnnntngan	ccntanntnn	cntatcaata	360
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nnnnnnnnntn	ggnttnnanc	annnnggntt	nnnnannggn	tttganccnn	tnnnncaaat	480
nngtnncan	tcngtnntan	atttannnn	naaaannncn	nanganntnn	tnaannnnat	540
ggatngnnntn	ngnaanngna	anacaaaaaa	agtnnanaan	aatggngtta	aagtnnnntt	600
nntnnnnnaa	ganganntnc	cnattnnng	ntcattnatg	gangatacnn	cnganncnaa	660
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ngtnntngtn	ccnntngcnt	atatnnantt	tgatgantan	tnnnnngaan	tnnannnnnga	780
nngnnnnnnn	tnnantaag	annnnnaanaa	agcnntnaan	ganatngana	aangccnga	840
naanaaaaaan	gcnnnnaana	annnnnnnaa	nntnnaanan	caantnnnng	cnaannanca	900

aaanntnnan gangnnannn nnntnnaann nnancatggn aangaattac cnatntcngc	960
ngnntncttn ntnatnaatc cntntgaagt ngtntantan gcnggtggna cntcnaatnn	1020
tnnnngncan ttngcnggna gntatgcnn ncaatggnnn atgattaant atgcnnnna	1080
ncatnnnatn nanngntana atttntatgg nnttagnggt nantttanng angangcnga	1140
agatgnnggn gtnntnaant taaaaaangg nttnnatgcn ganntnnntng antangttgg	1200
nganttnntn aaaccnatna anaancnnnt ntannnnnnn tatannncan taaaaaannt	1260
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19

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<213> artificial sequence
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1 5 10 15

48

gat aag atg cca tat agt cat ttc aca caa atg act gaa aac tat gag
Asp Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu
20 25 30

96

atg aaa gtt gca aat aaa aca gaa act cac tta gtt ggt ata aaa aat
Met Lys Val Ala Asn Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn
35 40 45

144

aaa gat aat gag gtt att gca gcc tgc atg ttg aca gca gta cca gtc
Lys Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val
50 55 60

192

atg aaa ttt ttt aag tac ttt tat tct aac cga gga cct gta att gat
Met Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp
65 70 75

240

tat gat aat aga gag ctt cac ttt ttc ttt aat gag tta aca aag
Tyr Asp Asn Arg Glu Leu Val His Phe Phe Asn Glu Leu Thr Lys
80 85 90 95

288

tat tta aaa cag cat aat tgt cta tat gtt cga gtt gac cct tat tta
Tyr Leu Lys Gln His Asn Cys Leu Tyr Val Arg Val Asp Pro Tyr Leu
100 105 110

336

cca tat caa tat tta aat cat gat ggt gaa att aca ggt aat gct ggt
Pro Tyr Gln Tyr Leu Asn His Asp Gly Glu Ile Thr Gly Asn Ala Gly

384

115	120	125	
aat gat tgg ttc ttt gat aag atg aag cat ctc gga ttt gaa cat gaa Asn Asp Trp Phe Phe Asp Lys Met Lys His Leu Gly Phe Glu His Glu 130	135	140	432
ggc ttt act aaa ggt ttt gat ccg att aaa caa atc cga tat cat tct Gly Phe Thr Lys Gly Phe Asp Pro Ile Lys Gln Ile Arg Tyr His Ser 145	150	155	480
gtt tta gat tta aaa aat aaa aca tct aaa gat ata tta aat gga atg Val Leu Asp Leu Lys Asn Lys Thr Ser Lys Asp Ile Leu Asn Gly Met 160	165	170	528
gat agt cta cgt aaa cgt aat act aaa gtt caa aaa aat ggt gtg Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val 180	185	190	576
aaa gtt aag ttc tta tca gaa gaa gaa ctt cca atc ttc cgt tca ttt Lys Val Lys Phe Leu Ser Glu Glu Leu Pro Ile Phe Arg Ser Phe 195	200	205	624
atg gaa gat aca acc gaa acg aaa gaa ttc caa gat aga gat gat agt Met Glu Asp Thr Thr Glu Thr Lys Glu Phe Gln Asp Arg Asp Asp Ser 210	215	220	672
ttc tat tat aat cgc tat aga cat ttc aaa gat cac gtg ctt gta cca Phe Tyr Tyr Asn Arg Tyr Arg His Phe Lys Asp His Val Leu Val Pro 225	230	235	720
cta gct tat att aag ttt gat gag tac atc gaa gaa tta caa aat gaa Leu Ala Tyr Ile Lys Phe Asp Glu Tyr Ile Glu Glu Leu Gln Asn Glu 240	245	250	768
cgt gaa act tta aat aaa gat gtt aat aaa gct tta aaa gat att gaa Arg Glu Thr Leu Asn Lys Asp Val Asn Lys Ala Leu Lys Asp Ile Glu 260	265	270	816
aaa cga cca gac aat aaa aag gca ttt aat aaa aaa gaa aat ctt gaa Lys Arg Pro Asp Asn Lys Lys Ala Phe Asn Lys Glu Asn Leu Glu 275	280	285	864
aaa caa tta gat gcc aat caa caa aaa tta gac gag gct aaa aaa tta Lys Gln Leu Asp Ala Asn Gln Gln Lys Leu Asp Glu Ala Lys Lys Leu 290	295	300	912
caa gcc gaa cat ggt aat gaa tta cca att tca gca ggt ttc ttc ttt Gln Ala Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe 305	310	315	960
att aat cca ttt gaa gtt gtt tat tat gca ggt gga act tct aat aaa Ile Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys 320	325	330	1008
tat aga cat ttt gca ggc agt tat gct att caa tgg aca atg att aac Tyr Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Thr Met Ile Asn 340	345	350	1056

tat gca att gat cat ggt att gat aga tac aat ttc tat ggt att agc Tyr Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser 355 360 365	1104
ggt aat ttt agt gaa gac gct gaa gat gtt gga gtc att aaa ttt aaa Gly Asn Phe Ser Glu Asp Ala Glu Asp Val Gly Val Ile Lys Phe Lys 370 375 380	1152
aaa ggt ttc aat gca gac gta att gag tat gtt gga gac ttt gtg aaa Lys Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys 385 390 395	1200
cct att aac aaa cct ttg tat tca gtg tat aag aca ctc aaa aag att Pro Ile Asn Lys Pro Leu Tyr Ser Val Tyr Lys Thr Leu Lys Lys Ile 400 405 410 415	1248
aaa aaa aga ttt aat taa agagggaaat agacgaatat gaaatttaca Lys Lys Arg Phe Asn 420	1296
gagttaaac	1305

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Lys Val Ala Asn Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn Lys 35 40 45

Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val Met 50 55 60

Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr 65 70 75 80
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Asp Asn Arg Glu Leu Val His Phe Phe Asn Glu Leu Thr Lys Tyr 85 90 95

Leu Lys Gln His Asn Cys Leu Tyr Val Arg Val Asp Pro Tyr Leu Pro 100 105 110
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Tyr Gln Tyr Leu Asn His Asp Gly Glu Ile Thr Gly Asn Ala Gly Asn
115 120 125

Asp Trp Phe Phe Asp Lys Met Lys His Leu Gly Phe Glu His Glu Gly
130 135 140

Phe Thr Lys Gly Phe Asp Pro Ile Lys Gln Ile Arg Tyr His Ser Val
145 150 155 160

Leu Asp Leu Lys Asn Lys Thr Ser Lys Asp Ile Leu Asn Gly Met Asp
165 170 175

Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
180 185 190

Val Lys Phe Leu Ser Glu Glu Leu Pro Ile Phe Arg Ser Phe Met
195 200 205

Glu Asp Thr Thr Glu Thr Lys Glu Phe Gln Asp Arg Asp Asp Ser Phe
210 215 220

Tyr Tyr Asn Arg Tyr Arg His Phe Lys Asp His Val Leu Val Pro Leu
225 230 235 240

Ala Tyr Ile Lys Phe Asp Glu Tyr Ile Glu Glu Leu Gln Asn Glu Arg
245 250 255

Glu Thr Leu Asn Lys Asp Val Asn Lys Ala Leu Lys Asp Ile Glu Lys
260 265 270

Arg Pro Asp Asn Lys Ala Phe Asn Lys Glu Asn Leu Glu Lys
275 280 285

Gln Leu Asp Ala Asn Gln Gln Lys Leu Asp Glu Ala Lys Lys Leu Gln
290 295 300

Ala Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Ile
305 310 315 320

Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys Tyr
325 330 335

Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Thr Met Ile Asn Tyr
340 345 350

Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
355 360 365

Asn Phe Ser Glu Asp Ala Glu Asp Val Gly Val Ile Lys Phe Lys Lys
370 375 380

Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys Pro
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Lys Arg Phe Asn
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Phe Thr Gln Met Thr Gly Asn Tyr Asn Leu Lys Val Ala Glu Lys Thr
20 25 30

gaa aca cat tta gtt ggt gtt aaa aat aat aat aac gaa gta att gca 144
Glu Thr His Leu Val Gly Val Lys Asn Asn Asn Glu Val Ile Ala
35 40 45

gca tgt tta ttg aca gct gta cca gtc atg aag ttt ttt aaa tac ttt 192
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
50 55 60

tac agc aat aga ggc cca gtt ata gat tat gct aac caa gaa ctt gta 240
Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Ala Asn Gln Glu Leu Val
65 70 75 80

cat ttt ttc ttt aat gag cta act aaa tat tta aaa aag tat aac tgt 288
His Phe Phe Asn Glu Leu Thr Lys Tyr Leu Lys Tyr Asn Cys

85	90	95	
ctc tat gtc cgc ata gat cca tac tta cct tat caa tat aga gac cat Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Tyr Arg Asp His 100	105	110	336
gac ggt aat ata acg gca aat gct ggc aat gat tgg ttt ttc aat aaa Asp Gly Asn Ile Thr Ala Asn Ala Gly Asn Asp Trp Phe Phe Asn Lys 115	120	125	384
atg gaa caa ctc gga tac cat cat gat ggc ttt aca aca gga ttt gat Met Glu Gln Leu Gly Tyr His His Asp Gly Phe Thr Thr Gly Phe Asp 130	135	140	432
cca ata tta caa atc aga ttc cat tct att ctt aat tta aag gat aag Pro Ile Leu Gln Ile Arg Phe His Ser Ile Leu Asn Leu Lys Asp Lys 145	150	155	480
aca gct aaa gat gtt tta aat aat atg gat agt tta cgt aaa aga aat Thr Ala Lys Asp Val Leu Asn Asn Met Asp Ser Leu Arg Lys Arg Asn 165	170	175	528
acc aaa aaa agt tca aaa aat gga gtc aaa gta aag ttc ctt act gaa Thr Lys Lys Ser Ser Lys Asn Gly Val Lys Val Lys Phe Leu Thr Glu 180	185	190	576
gaa gaa cta cct atc ttt cgt tca ttt atg gag cag acg tca gaa tct Glu Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Gln Thr Ser Glu Ser 195	200	205	624
aaa gaa ttc tct gat aga gac gac caa ttt tat tac aat cgg ttt aag Lys Glu Phe Ser Asp Arg Asp Asp Gln Phe Tyr Tyr Asn Arg Phe Lys 210	215	220	672
tac tat aaa gat agg gtg ctt gtg cct cta gca tat tta aaa ttt gat Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Leu Lys Phe Asp 225	230	235	720
gaa tat ata gaa gaa cta acg aat gaa cga caa act tta gaa aaa gat Glu Tyr Ile Glu Glu Leu Thr Asn Glu Arg Gln Thr Leu Glu Lys Asp 245	250	255	768
tta ggc aaa gca ctt aaa gac att gag aaa cga cca gat aac aaa aaa Leu Gly Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys 260	265	270	816
gct tat aat aaa cga gac aac cta caa caa ctc gat gcc aat caa Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Leu Asp Ala Asn Gln 275	280	285	864
caa aag tta aat gag gct aat cag tta caa gcg gaa cac ggt aat gag Gln Lys Leu Asn Glu Ala Asn Gln Leu Gln Ala Glu His Gly Asn Glu 290	295	300	912
tta cct atc tct gcc ggt ttc ttt att att aat ccg ttt gaa gtt gta Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val 305	310	315	960

tac tac gct gga ggt acc gct aat aaa tat cgt cat ttt gca ggt agt Tyr Tyr Ala Gly Gly Thr Ala Asn Lys Tyr Arg His Phe Ala Gly Ser 325	330	335	1008	
tac gcg gtt cag tgg act atg att aac tat gct atc gaa cac ggc ata Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr Ala Ile Glu His Gly Ile 340	345	350	1056	
gac aga tat aat ttc tac ggc att agt gga aac ttc tca gat gat gct Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asn Phe Ser Asp Asp Ala 355	360	365	1104	
gaa gac gca ggt gtc att cgc ttt aaa aaa ggt tat ggt gca gaa gtg Glu Asp Ala Gly Val Ile Arg Phe Lys Lys Gly Tyr Gly Ala Glu Val 370	375	380	1152	
att gaa tac gtt ggt gat ttt gta aaa cct ata aat aaa cct atg tat Ile Glu Tyr Val Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Met Tyr 385	390	395	400	1200
aaa ctt tat tca gtg tta aaa cga att caa aat aag cta tag Lys Leu Tyr Ser Val Leu Lys Arg Ile Gln Asn Lys Leu 405	410			1242
aggagaatgg attaattatg aaatttacag agtttaac				1280

<210> 43
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 <213> *Staphylococcus lugdunensis* femA

<400> 43

Thr Ala Asn Glu Phe Gly Asp Phe Thr Asp Gln Met Pro Tyr Ser His
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Phe Thr Gln Met Thr Gly Asn Tyr Asn Leu Lys Val Ala Glu Lys Thr
 20 25 30

Glu Thr His Leu Val Gly Val Lys Asn Asn Asn Asn Glu Val Ile Ala
 35 40 45

Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
 50 55 60

Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Ala Asn Gln Glu Leu Val
 65 70 75 80

His Phe Phe Phe Asn Glu Leu Thr Lys Tyr Leu Lys Lys Tyr Asn Cys
 85 90 95

Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Tyr Arg Asp His
100 105 110

Asp Gly Asn Ile Thr Ala Asn Ala Gly Asn Asp Trp Phe Phe Asn Lys
115 120 125

Met Glu Gln Leu Gly Tyr His His Asp Gly Phe Thr Thr Gly Phe Asp
130 135 140

Pro Ile Leu Gln Ile Arg Phe His Ser Ile Leu Asn Leu Lys Asp Lys
145 150 155 160

Thr Ala Lys Asp Val Leu Asn Asn Met Asp Ser Leu Arg Lys Arg Asn
165 170 175

Thr Lys Lys Ser Ser Lys Asn Gly Val Lys Val Lys Phe Leu Thr Glu
180 185 190

Glu Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Gln Thr Ser Glu Ser
195 200 205

Lys Glu Phe Ser Asp Arg Asp Asp Gln Phe Tyr Tyr Asn Arg Phe Lys
210 215 220

Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Leu Lys Phe Asp
225 230 235 240

Glu Tyr Ile Glu Glu Leu Thr Asn Glu Arg Gln Thr Leu Glu Lys Asp
245 250 255

Leu Gly Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys
260 265 270

Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Gln Leu Asp Ala Asn Gln
275 280 285

Gln Lys Leu Asn Glu Ala Asn Gln Leu Gln Ala Glu His Gly Asn Glu
290 295 300

Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
305 310 315 320

Tyr Tyr Ala Gly Gly Thr Ala Asn Lys Tyr Arg His Phe Ala Gly Ser
325 330 335

Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr Ala Ile Glu His Gly Ile
340 345 350

Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asn Phe Ser Asp Asp Ala
355 360 365

Glu Asp Ala Gly Val Ile Arg Phe Lys Lys Gly Tyr Gly Ala Glu Val
370 375 380

Ile Glu Tyr Val Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Met Tyr
385 390 395 400

Lys Leu Tyr Ser Val Leu Lys Arg Ile Gln Asn Lys Leu
405 410

<210> 44

<211> 1295

<212> DNA

<213> *Staphylococcus xylosus* femA

<220>

<221> CDS

<222> (1)..(1245)

<400> 44

acg caa aag agt ttg ggt gca ttt tca gat aaa atg cca aat agc cat
Thr Gln Lys Ser Leu Gly Ala Phe Ser Asp Lys Met Pro Asn Ser His
1 5 10 15

48

ttc acg caa atg gta ggg aat tat gaa ttg aaa att gca gaa agt act
Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Ile Ala Glu Ser Thr
20 25 30

96

gaa aca cat tta gta ggt ata aaa aac aat gat aat gaa gtc att gca
Glu Thr His Leu Val Gly Ile Lys Asn Asn Asp Asn Glu Val Ile Ala
35 40 45

144

gct tgt tta tta act gca gta cca gta atg aaa ttc ttt aag tat ttt
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
50 55 60

192

tat act aat aga ggt ccg gtt ata gat ttt gaa aat aaa gaa tta gtg
Tyr Thr Asn Arg Gly Pro Val Ile Asp Phe Glu Asn Lys Glu Leu Val
65 70 75 80

240

cat tac ttt ttc aat gaa cta tct aaa tat gtg aaa aaa cat aat gcg
His Tyr Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Ala

288

85	90	95	
ctt tat tta aga gtt gat cct tat tta gca tat caa tac cgt aat cat Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala Tyr Gln Tyr Arg Asn His 100	105	110	336
gat ggt gag gta ttg gaa aat gca gga cat gat tgg att ttc gat aaa Asp Gly Glu Val Leu Glu Asn Ala Gly His Asp Trp Ile Phe Asp Lys 115	120	125	384
atg aag cag ctt gga tat aaa cac caa gga ttt tta act ggt ttc gat Met Lys Gln Leu Gly Tyr Lys His Gln Gly Phe Leu Thr Gly Phe Asp 130	135	140	432
tca att att caa att agg ttc cac tct gta ctg gat tta gta ggt aaa Ser Ile Ile Gln Ile Arg Phe His Ser Val Leu Asp Leu Val Gly Lys 145	150	155	480
act gct aaa gat gta cta aat ggt atg gat agt tta cgt aaa cgt aat Thr Ala Lys Asp Val Leu Asn Gly Met Asp Ser Leu Arg Lys Arg Asn 165	170	175	528
act aaa aaa gta caa aaa aat ggc gtg aaa gta agg ttc tta agg gaa Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Arg Glu 180	185	190	576
gat gag ttg cca att ttc cgt tca ttc atg gaa gat aca tct gaa act Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr 195	200	205	624
aaa gac ttt gac gat aga gac gat ggc ttt tac tac aat aga tta agg Lys Asp Phe Asp Asp Arg Asp Asp Gly Phe Tyr Tyr Asn Arg Leu Arg 210	215	220	672
tat tat aaa gat cgc gta tta gta cct cta gct tat atg gat ttc aat Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Met Asp Phe Asn 225	230	235	720
gaa tat att gaa gaa ttg caa gct gaa cgt gag gtg tta agc aaa gat Glu Tyr Ile Glu Glu Leu Gln Ala Glu Arg Glu Val Leu Ser Lys Asp 245	250	255	768
atc aat aaa gca gta aaa gat atc gag aaa aga cct gaa aat aaa aaa Ile Asn Lys Ala Val Lys Asp Ile Glu Lys Arg Pro Glu Asn Lys Lys 260	265	270	816
gca tat aat aaa aaa gat aat cta gag aaa caa ctt ata gcg aat caa Ala Tyr Asn Lys Lys Asp Asn Leu Glu Lys Gln Leu Ile Ala Asn Gln 275	280	285	864
caa aaa att gat gaa gct aaa act cta caa gag aag cat ggt aac gaa Gln Lys Ile Asp Glu Ala Lys Thr Leu Gln Glu Lys His Gly Asn Glu 290	295	300	912
cta cca atc tca gca gca tat ttc atc att aac cct tat gaa gta gtg Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile Asn Pro Tyr Glu Val Val 305	310	315	960
		320	

tat tat gct ggt gga acg tca aat gag ttt aga cat ttt gct ggt agt 1008
Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe Arg His Phe Ala Gly Ser
325 330 335

tat gcc att caa tgg aag atg att aac tat gct att gac cat aat att 1056
Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Ile Asp His Asn Ile
340 345 350

gat aga tat aat ttt tat gga att agt ggt cat ttt aca gaa gat gca 1104
Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly His Phe Thr Glu Asp Ala
355 360 365

gaa gat gcc ggt gta gtt aaa ttt aaa aaa gga ttt aat gct gat gta 1152
Glu Asp Ala Gly Val Val Lys Phe Lys Lys Gly Phe Asn Ala Asp Val
370 375 380

gtg gaa tat gtt ggt gat ttt att aaa cca atc aat aaa cca atg tac 1200
Val Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
385 390 395 400

aaa att tat acg aca tta aag aaa att aaa gat aaa aag aaa taa 1245
Lys Ile Tyr Thr Leu Lys Ile Lys Asp Lys Lys Lys
405 410

acatttaata gaaggaaact aagctagaat gaaatttaca gagttaaacc 1295

<210> 45
<211> 414
<212> PRT
<213> *Staphylococcus xylosus* femA

<400> 45

Thr Gln Lys Ser Leu Gly Ala Phe Ser Asp Lys Met Pro Asn Ser His
1 5 10 15

Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Ile Ala Glu Ser Thr
20 25 30

Glu Thr His Leu Val Gly Ile Lys Asn Asn Asp Asn Glu Val Ile Ala
35 40 45

Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
50 55 60

Tyr Thr Asn Arg Gly Pro Val Ile Asp Phe Glu Asn Lys Glu Leu Val
65 70 75 80

His Tyr Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Ala
85 90 95

Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala Tyr Gln Tyr Arg Asn His
100 105 110

Asp Gly Glu Val Leu Glu Asn Ala Gly His Asp Trp Ile Phe Asp Lys
115 120 125

Met Lys Gln Leu Gly Tyr Lys His Gln Gly Phe Leu Thr Gly Phe Asp
130 135 140

Ser Ile Ile Gln Ile Arg Phe His Ser Val Leu Asp Leu Val Gly Lys
145 150 155 160

Thr Ala Lys Asp Val Leu Asn Gly Met Asp Ser Leu Arg Lys Arg Asn
165 170 175

Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Arg Glu
180 185 190

Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
195 200 205

Lys Asp Phe Asp Asp Arg Asp Asp Gly Phe Tyr Tyr Asn Arg Leu Arg
210 215 220

Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Met Asp Phe Asn
225 230 235 240

Glu Tyr Ile Glu Glu Leu Gln Ala Glu Arg Glu Val Leu Ser Lys Asp
245 250 255

Ile Asn Lys Ala Val Lys Asp Ile Glu Lys Arg Pro Glu Asn Lys Lys
260 265 270

Ala Tyr Asn Lys Lys Asp Asn Leu Glu Lys Gln Leu Ile Ala Asn Gln
275 280 285

Gln Lys Ile Asp Glu Ala Lys Thr Leu Gln Glu Lys His Gly Asn Glu
290 295 300

Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile Asn Pro Tyr Glu Val Val
305 310 315 320

Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe Arg His Phe Ala Gly Ser
325 330 335

Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Ile Asp His Asn Ile
340 345 350

Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly His Phe Thr Glu Asp Ala
355 360 365

Glu Asp Ala Gly Val Val Lys Phe Lys Lys Gly Phe Asn Ala Asp Val
370 375 380

Val Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
385 390 395 400

Lys Ile Tyr Thr Leu Lys Lys Ile Lys Asp Lys Lys Lys
405 410

<210> 46

<211> 1283

<212> DNA

<213> *Staphylococcus capitis* femA

<220>

<221> CDS

<222> (1)..(1236)

<400> 46
aca gct aaa gaa ttt agt gac ttt act gat caa atg cct tat agc cat 48
Thr Ala Lys Glu Phe Ser Asp Phe Thr Asp Gln Met Pro Tyr Ser His
1 5 10 15

ttt act cag atg gaa ggt aat tat gaa ctt aaa gtt gct gaa ggt acg 96
Phe Thr Gln Met Glu Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Thr
20 25 30

gat tca cat ctc gta gga att aaa aat aat gac aac caa gtg att gca 144
Asp Ser His Leu Val Gly Ile Lys Asn Asn Asp Asn Gln Val Ile Ala
35 40 45

gca tgt tta tta act gct gta cct gta atg aaa att ttt aaa tat ttt 192
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Ile Phe Lys Tyr Phe
50 55 60

tac tca aat cgc ggg cca gtg att gat tat gat aat aaa gag ctt gtt 240
Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Asp Asn Lys Glu Leu Val
65 70 75 80

cac ttt ttc ttt aat gaa tta agt aaa tat gta aaa aag cat aat tgt 288
His Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Cys

85	90	95	
ctt tat cta aga gtt gac cct tat ctt cct tat caa tac tta aat cat Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Tyr Gln Tyr Leu Asn His 100	105	110	336
gac ggt gaa att att gga aat gct ggc cat gat tgg ttt ttc aat aag Asp Gly Glu Ile Ile Gly Asn Ala Gly His Asp Trp Phe Phe Asn Lys 115	120	125	384
atg gaa gaa tta gga ttt gaa cat gaa ggc ttt cat aaa ggc ttc cat Met Glu Glu Leu Gly Phe Glu His Glu Gly Phe His Lys Gly Phe His 130	135	140	432
cct atc tta caa gta aga tat cat tca gtt tta gat tta aaa gat aaa Pro Ile Leu Gln Val Arg Tyr His Ser Val Leu Asp Leu Lys Asp Lys 145	150	155	480
acg gct aaa gat gta ctc aaa gga atg gat agt tta aga aag cgt aat Thr Ala Lys Asp Val Leu Lys Gly Met Asp Ser Leu Arg Lys Arg Asn 165	170	175	528
act aag aaa gta caa aaa aat ggt gtc aaa gtc cgt ttc cta tcc gaa Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Glu 180	185	190	576
gat gaa tta cct atc ttt aga tca ttt atg gaa gat act aca gaa acg Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Thr Glu Thr 195	200	205	624
aaa gag ttc gcc gat aga gat gat agt ttc tat tat aat cga tta aaa Lys Glu Phe Ala Asp Arg Asp Ser Phe Tyr Tyr Asn Arg Leu Lys 210	215	220	672
tac ttt aaa gat aga gta tta gta cca tta gca tat gtt gac ttc gat Tyr Phe Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Val Asp Phe Asp 225	230	235	720
gag tat att gaa gaa ctt aat aat gaa aga gat gtt ctt aat aaa gat Glu Tyr Ile Glu Glu Leu Asn Asn Glu Arg Asp Val Leu Asn Lys Asp 245	250	255	768
tta aat aag gcg ctc aaa gat att gag aag aga cct gat aat aag aaa Leu Asn Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys 260	265	270	816
gct tat aac aaa aga gat aat ctt caa caa caa tta gat gca aat caa Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Leu Asp Ala Asn Gln 275	280	285	864
caa aaa att gat gaa gct aaa aac tta caa caa gaa cat ggt aat gaa Gln Lys Ile Asp Glu Ala Lys Asn Leu Gln Gln Glu His Gly Asn Glu 290	295	300	912
tta cct att tca gct gga tat ttc ttc att aat ccg ttt gaa gtt gtt Leu Pro Ile Ser Ala Gly Tyr Phe Phe Ile Asn Pro Phe Glu Val Val 305	310	315	960

tat tac gca ggt ggc aca tcg aat cgt tat cgt cac tat gcc gga agt Tyr Tyr Ala Gly Gly Thr Ser Asn Arg Tyr Arg His Tyr Ala Gly Ser 325	330	335	1008	
tat gca att caa tgg aaa atg ata aac tat gct tta gaa cat gga att Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Leu Glu His Gly Ile 340	345	350	1056	
aac cgt tat aat ttt tat gga gtt agt ggg gac ttc agt gaa gac gct Asn Arg Tyr Asn Phe Tyr Gly Val Ser Gly Asp Phe Ser Glu Asp Ala 355	360	365	1104	
gaa gat gta gga gta att aag ttc aaa aaa ggc tat aat gct gat gtt Glu Asp Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val 370	375	380	1152	
att gaa tat gta ggt gat ttt atc aag cca atc aat aaa cct atg tat Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr 385	390	395	400	1200
gca atc tat aac gca ctt aaa aag tta aag aaa tag attttttac Ala Ile Tyr Asn Ala Leu Lys Lys Leu Lys Lys 405	410			1246
caacccaatt atctaattat gaaatttaca gagttaa				1283
<210> 47				
<211> 411				
<212> PRT				
<213> <i>Staphylococcus capitis</i> femA				
<400> 47				
Thr Ala Lys Glu Phe Ser Asp Phe Thr Asp Gln Met Pro Tyr Ser His 1	5	10	15	
Phe Thr Gln Met Glu Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Thr 20	25	30		
Asp Ser His Leu Val Gly Ile Lys Asn Asn Asp Asn Gln Val Ile Ala 35	40	45		
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Ile Phe Lys Tyr Phe 50	55	60		
Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Asp Asn Lys Glu Leu Val 65	70	75	80	
His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Cys 85	90	95		

Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Tyr Gln Tyr Leu Asn His
100 105 110

Asp Gly Glu Ile Ile Gly Asn Ala Gly His Asp Trp Phe Phe Asn Lys
115 120 125

Met Glu Glu Leu Gly Phe Glu His Glu Gly Phe His Lys Gly Phe His
130 135 140

Pro Ile Leu Gln Val Arg Tyr His Ser Val Leu Asp Leu Lys Asp Lys
145 150 155 160

Thr Ala Lys Asp Val Leu Lys Gly Met Asp Ser Leu Arg Lys Arg Asn
165 170 175

Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Glu
180 185 190

Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Thr Glu Thr
195 200 205

Lys Glu Phe Ala Asp Arg Asp Asp Ser Phe Tyr Tyr Asn Arg Leu Lys
210 215 220

Tyr Phe Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Val Asp Phe Asp
225 230 235 240

Glu Tyr Ile Glu Glu Leu Asn Asn Glu Arg Asp Val Leu Asn Lys Asp
245 250 255

Leu Asn Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys
260 265 270

Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Leu Asp Ala Asn Gln
275 280 285

Gln Lys Ile Asp Glu Ala Lys Asn Leu Gln Gln Glu His Gly Asn Glu
290 295 300

Leu Pro Ile Ser Ala Gly Tyr Phe Phe Ile Asn Pro Phe Glu Val Val
305 310 315 320

Tyr Tyr Ala Gly Gly Thr Ser Asn Arg Tyr Arg His Tyr Ala Gly Ser
325 330 335

Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Leu Glu His Gly Ile
340 345 350

Asn Arg Tyr Asn Phe Tyr Gly Val Ser Gly Asp Phe Ser Glu Asp Ala
355 360 365

Glu Asp Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val
370 375 380

Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
385 390 395 400

Ala Ile Tyr Asn Ala Leu Lys Lys Leu Lys Lys
405 410

<210> 48

<211> 1297

<212> DNA

<213> *Staphylococcus schleiferi* femA

<220>

<221> CDS

<222> (1)..(1248)

<400> 48

acg acg gct gaa ttt ggt gcg ttt aca gat caa atg cca tat agc cat
Thr Thr Ala Glu Phe Gly Ala Phe Thr Asp Gln Met Pro Tyr Ser His
1 5 10 15

ttc acg caa atg gta ggg aac tat gaa tta aag gtt gct gaa ggt gtt
Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Val
20 25 30 96

gaa aca cat ctt gtc ggc att aaa gat aac aac aat aac gta cta gca
Glu Thr His Leu Val Gly Ile Lys Asp Asn Asn Asn Val Leu Ala
35 40 45 144

gca tgt tta ctg aca gca gtg cca gta atg aag ttt ttt aaa tat ttt
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
50 55 60 192

tat tca aac cgc gga cca gtc atg gac tac gaa aat aaa gag ctc gtt
Tyr Ser Asn Arg Gly Pro Val Met Asp Tyr Glu Asn Lys Glu Leu Val
65 70 75 80 240

cat ttc ttt ttt aat gaa ctt tca aaa tat gtt aag aaa tat cac gca
His Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys Tyr His Ala
288

85	90	95	
ttg tat ttg aga gta gac cct tat tta cca atg tta aag cga aac cat Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Met Leu Lys Arg Asn His 100	105	110	336
gat ggt gaa gtg att gaa aga tac ggc agt gac tgg ttt ttt gat aaa Asp Gly Glu Val Ile Glu Arg Tyr Gly Ser Asp Trp Phe Phe Asp Lys 115	120	125	384
atg gct gaa tta aac ttt gaa cat gaa ggt ttc aca act ggg ttt gat Met Ala Glu Leu Asn Phe Glu His Glu Gly Phe Thr Thr Gly Phe Asp 130	135	140	432
aca ata agg caa att cgt ttt cat tct gtg ctc gat gtt gaa aat aaa Thr Ile Arg Gln Ile Arg Phe His Ser Val Leu Asp Val Glu Asn Lys 145	150	155	480
aca tca aaa gac atc tta aat caa atg gat aat tta agg aaa aga aat Thr Ser Lys Asp Ile Leu Asn Gln Met Asp Asn Leu Arg Lys Arg Asn 165	170	175	528
acg aaa aaa gta cag aaa aat ggt gtg aaa gtc cgc tat cta aac gaa Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Tyr Leu Asn Glu 180	185	190	576
gat gaa tta cat att ttc cgt tcg ttt atg gaa gat aca tct gaa aca Asp Glu Leu His Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr 195	200	205	624
aaa gat ttt gta gat aga gat gac gat ttt tat tat cat cgt atg aaa Lys Asp Phe Val Asp Arg Asp Asp Phe Tyr Tyr His Arg Met Lys 210	215	220	672
tac tat aaa gat cgt gtc cgc gta cca cta gcg tat att gat ttt aat Tyr Tyr Lys Asp Arg Val Arg Val Pro Leu Ala Tyr Ile Asp Phe Asn 225	230	235	720
gca tat tta gca gag ctc aac act gaa gcg caa gac ttt aaa aaa gaa Ala Tyr Leu Ala Glu Leu Asn Thr Glu Ala Gln Asp Phe Lys Lys Glu 245	250	255	768
att gca aaa gca gat aaa gac atc gac aag cgt cct gaa aat cag aaa Ile Ala Lys Ala Asp Lys Asp Ile Asp Lys Arg Pro Glu Asn Gln Lys 260	265	270	816
gcc ata aat aaa aag aaa aat tta gag caa caa cta gaa gcg aat caa Ala Ile Asn Lys Lys Asn Leu Glu Gln Gln Leu Glu Ala Asn Gln 275	280	285	864
gct aaa ata aaa gaa gca gaa aca ttg caa ctt aaa cac ggt gac aca Ala Lys Ile Lys Glu Ala Glu Thr Leu Gln Leu Lys His Gly Asp Thr 290	295	300	912
tta ccg att tcg gct gga ttc ttt att att aat cca ttt gag gtt gtt Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val 305	310	315	960
		320	

tat tat gca ggc ggc aca gca aac gaa ttt cgt cat ttt gct gga agc 1008
Tyr Tyr Ala Gly Gly Thr Ala Asn Glu Phe Arg His Phe Ala Gly Ser
325 330 335

tac gca gtg caa tgg gaa atg att aat tat gcg att gat tat caa att 1056
Tyr Ala Val Gln Trp Glu Met Ile Asn Tyr Ala Ile Asp Tyr Gln Ile
340 345 350

cca aga tat aac ttt tat ggc att agt ggt gat ttt tca gaa gat gca 1104
Pro Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala
355 360 365

gaa gat gca ggt gtg ata aaa ttt aaa aaa ggc tat aat gca gaa gta 1152
Glu Asp Ala Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Glu Val
370 375 380

ata gaa tat gtc ggt gat ttt att aag cct ata aac aaa cct gcc tat 1200
Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Ala Tyr
385 390 395 400

aca gtc tac tta aaa tta aag caa tta aaa gac aag ata aaa aga taa 1248
Thr Val Tyr Leu Lys Leu Lys Gln Leu Lys Asp Lys Ile Lys Arg
405 410 415

gatatagcaa agagaagggg atttattggt atgaaattta cagagttaa 1297

<210> 49
<211> 415
<212> PRT
<213> *Staphylococcus schleiferi* femA

<400> 49

Thr Thr Ala Glu Phe Gly Ala Phe Thr Asp Gln Met Pro Tyr Ser His
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Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Val
20 25 30

Glu Thr His Leu Val Gly Ile Lys Asp Asn Asn Asn Val Leu Ala
35 40 45

Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
50 55 60

Tyr Ser Asn Arg Gly Pro Val Met Asp Tyr Glu Asn Lys Glu Leu Val
65 70 75 80

His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys Tyr His Ala
85 90 95

Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Met Leu Lys Arg Asn His
100 105 110

Asp Gly Glu Val Ile Glu Arg Tyr Gly Ser Asp Trp Phe Phe Asp Lys
115 120 125

Met Ala Glu Leu Asn Phe Glu His Glu Gly Phe Thr Thr Gly Phe Asp
130 135 140

Thr Ile Arg Gln Ile Arg Phe His Ser Val Leu Asp Val Glu Asn Lys
145 150 155 160

Thr Ser Lys Asp Ile Leu Asn Gln Met Asp Asn Leu Arg Lys Arg Asn
165 170 175

Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Tyr Leu Asn Glu
180 185 190

Asp Glu Leu His Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
195 200 205

Lys Asp Phe Val Asp Arg Asp Asp Phe Tyr Tyr His Arg Met Lys
210 215 220

Tyr Tyr Lys Asp Arg Val Arg Val Pro Leu Ala Tyr Ile Asp Phe Asn
225 230 235 240

Ala Tyr Leu Ala Glu Leu Asn Thr Glu Ala Gln Asp Phe Lys Lys Glu
245 250 255

Ile Ala Lys Ala Asp Lys Asp Ile Asp Lys Arg Pro Glu Asn Gln Lys
260 265 270

Ala Ile Asn Lys Lys Asn Leu Glu Gln Gln Leu Glu Ala Asn Gln
275 280 285

Ala Lys Ile Lys Glu Ala Glu Thr Leu Gln Leu Lys His Gly Asp Thr
290 295 300

Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
305 310 315 320

Tyr Tyr Ala Gly Gly Thr Ala Asn Glu Phe Arg His Phe Ala Gly Ser
325 330 335

Tyr Ala Val Gln Trp Glu Met Ile Asn Tyr Ala Ile Asp Tyr Gln Ile
340 345 350

Pro Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala
355 360 365

Glu Asp Ala Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Glu Val
370 375 380

Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Ala Tyr
385 390 395 400

Thr Val Tyr Leu Lys Leu Lys Gln Leu Lys Asp Lys Ile Lys Arg
405 410 415

<210> 50

<211> 1284

<212> DNA

<213> *Staphylococcus sciuri* femA

<220>

<221> CDS

<222> (1)..(1233)

<400> 50
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Thr Leu Glu Phe Glu Ala Phe Thr Asn Lys Met Pro Tyr Ala His Phe
1 5 10 15

aca caa gca gta ggt aat tat gaa tta aaa aca tct gaa ggt act tca 96
Thr Gln Ala Val Gly Asn Tyr Glu Leu Lys Thr Ser Glu Gly Thr Ser
20 25 30

aca cat tta gta ggg gtc aaa gat aat caa ggt gaa gta tta gct gcg 144
Thr His Leu Val Gly Val Lys Asp Asn Gln Gly Glu Val Leu Ala Ala
35 40 45

tgt ctg tta aca agt gta cca gtt atg aag aaa ttt aat tac ttt tac 192
Cys Leu Leu Thr Ser Val Pro Val Met Lys Lys Phe Asn Tyr Phe Tyr
50 55 60

tca aat aga gga cca gta atg gat tat gac aac aaa gaa ctt gtt gac 240
Ser Asn Arg Gly Pro Val Met Asp Tyr Asp Asn Lys Glu Leu Val Asp
65 70 75 80

ttt ttc ttt aaa gaa atc gtg agc tat tta aaa agt tat aaa gga tta 288
Phe Phe Phe Lys Glu Ile Val Ser Tyr Leu Lys Ser Tyr Lys Gly Leu

85	90	95	
ttc ttt aga atc gat cct tac ttg cca tat caa cta aga gat cat gat Phe Phe Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Leu Arg Asp His Asp 100	105	110	336
ggc aat att aaa aaa tca ttc aac cgt gat ggt tta att aaa caa ttt Gly Asn Ile Lys Lys Ser Phe Asn Arg Asp Gly Leu Ile Lys Gln Phe 115	120	125	384
gaa tca tta ggt tat gaa cac caa ggc ttc aca act ggt ttc cac cca Glu Ser Leu Gly Tyr Glu His Gln Gly Phe Thr Thr Gly Phe His Pro 130	135	140	432
ata cat caa att aga tgg cat tct gta ctt gat tta gaa agt atg gac Ile His Gln Ile Arg Trp His Ser Val Leu Asp Leu Glu Ser Met Asp 145	150	155	480
gaa aag acg ctc atc aag aac atg gac agt tta aga aaa aga aat act Glu Lys Thr Leu Ile Lys Asn Met Asp Ser Leu Arg Lys Arg Asn Thr 165	170	175	528
aaa aaa gtt caa aaa aat ggt gtt aaa gtt cgt ttt cta tct aaa gat Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Lys Asp 180	185	190	576
gaa atg ccg ata ttc cgt caa ttt atg gaa gat act aca gag aag aaa Glu Met Pro Ile Phe Arg Gln Phe Met Glu Asp Thr Thr Glu Lys Lys 195	200	205	624
gat ttc aac gat cgt ggc gat gac ttc tat tac aat aga tta aaa tac Asp Phe Asn Asp Arg Gly Asp Asp Phe Tyr Tyr Asn Arg Leu Lys Tyr 210	215	220	672
ttt gaa aat gta aag att cct tta gca tat ata gac ttt gaa act tac Phe Glu Asn Val Lys Ile Pro Leu Ala Tyr Ile Asp Phe Glu Thr Tyr 225	230	235	720
att cca caa tta gaa aaa gaa cat gaa caa tac aac aaa gat att gca Ile Pro Gln Leu Glu Lys His Glu Gln Tyr Asn Lys Asp Ile Ala 245	250	255	768
aaa gct gaa aaa gat tta gaa aag aaa cca gat aat caa aaa acg att Lys Ala Glu Lys Asp Leu Glu Lys Lys Pro Asp Asn Gln Lys Thr Ile 260	265	270	816
aat aaa ata gac aac tta aaa caa caa aga gaa gca aat gaa gct aaa Asn Lys Ile Asp Asn Leu Lys Gln Gln Arg Glu Ala Asn Glu Ala Lys 275	280	285	864
tta gaa gaa gca ctt caa cta caa gaa cat ggt gat aca tta cca Leu Glu Glu Ala Leu Gln Leu Gln Gln Glu His Gly Asp Thr Leu Pro 290	295	300	912
ata gca gct ggt ttc ttt att att aat cca ttt gaa gtt gta tat tat Ile Ala Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val Tyr Tyr 305	310	315	960

gca ggt ggt tca tcg aat gaa tat cgt cac ttt gca ggt agt tat gca Ala Gly Gly Ser Ser Asn Glu Tyr Arg His Phe Ala Gly Ser Tyr Ala 325 330 335	1008
att cag tgg gaa atg att aaa tac gcg tta gat cac aac att gac cgt Ile Gln Trp Glu Met Ile Lys Tyr Ala Leu Asp His Asn Ile Asp Arg 340 345 350	1056
tat aac ttc tat ggt atc agc gga gac ttc tca gaa gat gca cct gat Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala Pro Asp 355 360 365	1104
gtt ggc gtt att aaa ttt aaa aaa ggt tac aat gca gat gtt tat gaa Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val Tyr Glu 370 375 380	1152
tat att ggt gat ttc gtt aaa cca att aat aaa cca gcg tac aaa gca Tyr Ile Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Ala Tyr Lys Ala 385 390 395 400	1200
tat aca aca cta aaa aaa gta tta aaa aaa taa atgatttca gtaagagagg Tyr Thr Thr Leu Lys Lys Val Leu Lys Lys 405 410	1253
aat tagata atatgaaatt tacagagtta a	1284

<210> 51
 <211> 410
 <212> PRT
 <213> *Staphylococcus sciuri* femA

<400> 51

Thr Leu Glu Phe Glu Ala Phe Thr Asn Lys Met Pro Tyr Ala His Phe
 1 5 10 15

Thr Gln Ala Val Gly Asn Tyr Glu Leu Lys Thr Ser Glu Gly Thr Ser
 20 25 30

Thr His Leu Val Gly Val Lys Asp Asn Gln Gly Glu Val Leu Ala Ala
 35 40 45

Cys Leu Leu Thr Ser Val Pro Val Met Lys Lys Phe Asn Tyr Phe Tyr
 50 55 60

Ser Asn Arg Gly Pro Val Met Asp Tyr Asp Asn Lys Glu Leu Val Asp
 65 70 75 80

Phe Phe Phe Lys Glu Ile Val Ser Tyr Leu Lys Ser Tyr Lys Gly Leu
 85 90 95

Phe Phe Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Leu Arg Asp His Asp
100 105 110

Gly Asn Ile Lys Lys Ser Phe Asn Arg Asp Gly Leu Ile Lys Gln Phe
115 120 125

Glu Ser Leu Gly Tyr Glu His Gln Gly Phe Thr Thr Gly Phe His Pro
130 135 140

Ile His Gln Ile Arg Trp His Ser Val Leu Asp Leu Glu Ser Met Asp
145 150 155 160

Glu Lys Thr Leu Ile Lys Asn Met Asp Ser Leu Arg Lys Arg Asn Thr
165 170 175

Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Lys Asp
180 185 190

Glu Met Pro Ile Phe Arg Gln Phe Met Glu Asp Thr Thr Glu Lys Lys
195 200 205

Asp Phe Asn Asp Arg Gly Asp Asp Phe Tyr Tyr Asn Arg Leu Lys Tyr
210 215 220

Phe Glu Asn Val Lys Ile Pro Leu Ala Tyr Ile Asp Phe Glu Thr Tyr
225 230 235 240

Ile Pro Gln Leu Glu Lys Glu His Gln Tyr Asn Lys Asp Ile Ala
245 250 255

Lys Ala Glu Lys Asp Leu Glu Lys Lys Pro Asp Asn Gln Lys Thr Ile
260 265 270

Asn Lys Ile Asp Asn Leu Lys Gln Gln Arg Glu Ala Asn Glu Ala Lys
275 280 285

Leu Glu Glu Ala Leu Gln Leu Gln Gln Glu His Gly Asp Thr Leu Pro
290 295 300

Ile Ala Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val Tyr Tyr
305 310 315 320

Ala Gly Gly Ser Ser Asn Glu Tyr Arg His Phe Ala Gly Ser Tyr Ala
325 330 335

Ile Gln Trp Glu Met Ile Lys Tyr Ala Leu Asp His Asn Ile Asp Arg
340 345 350

Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala Pro Asp
355 360 365

Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val Tyr Glu
370 375 380

Tyr Ile Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Ala Tyr Lys Ala
385 390 395 400

Tyr Thr Thr Leu Lys Lys Val Leu Lys Lys
405 410

<210> 52

<211> 1343

<212> DNA

<213> *Staphylococcus hominis* femA

<220>

<221> CDS

<222> (64)..(1317)

<400> 52

taaaatttta aaatttagtca actcaaatta aataaagatt ctaaatttagg agttatagag 60

ata atg aag ttt aca aat tta aca gct aca gaa ttt ggc gat ttt act 108
Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asp Phe Thr
1 5 10 15

gaa aaa atg cca tat agc cat ttt aca cag atg act gaa aat tat gag 156
Glu Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu
20 25 30

tta aaa gtt gct gag aaa act gaa act cat tta gta gga att aaa aat 204
Leu Lys Val Ala Glu Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn
35 40 45

aaa gat aat gaa gtc att gct gct tgt atg cta act gct gta ccc gtt 252
Lys Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val
50 55 60

atg aaa att ttt aaa tat ttt tat tca aat cgt ggt cca gtc att gat 300
Met Lys Ile Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp
65 70 75

tat gaa aac aaa gaa ctc gtt cac ttt ttc ttt aac gaa tta agt aaa Tyr Glu Asn Lys Glu Leu Val His Phe Phe Phe Asn Glu Leu Ser Lys 80 85 90 95	348
tat tta aaa caa caa cat tgt tta tat gta cgt ata gac cct tat ttg Tyr Leu Lys Gln Gln His Cys Leu Tyr Val Arg Ile Asp Pro Tyr Leu 100 105 110	396
cct tat caa tat cgt aat cat gat ggt gat att aca gga aat gct ggg Pro Tyr Gln Tyr Arg Asn His Asp Gly Asp Ile Thr Gly Asn Ala Gly 115 120 125	444
aat gat tgg ttc ttc gat aaa atg aaa caa tta gga tat caa cac gaa Asn Asp Trp Phe Phe Asp Lys Met Lys Gln Leu Gly Tyr Gln His Glu 130 135 140	492
ggg ttt aca aca gga ttt gat cca ata tta caa att cgg ttc cat tca Gly Phe Thr Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser 145 150 155	540
gtt tta aat tta aag gat aaa act gct aaa gat gta tta aat gga atg Val Leu Asn Leu Lys Asp Lys Thr Ala Lys Asp Val Leu Asn Gly Met 160 165 170 175	588
gat agt tta cga aaa aga aat act aaa aaa gtc caa aaa aat ggt gtt Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val 180 185 190	636
aaa gta aga ttt ctt act aaa gaa gaa tta cct att ttc aga tca ttt Lys Val Arg Phe Leu Thr Lys Glu Leu Pro Ile Phe Arg Ser Phe 195 200 205	684
atg gaa gat aca tca gag act aaa gaa ttt tct gat aga gag gat agt Met Glu Asp Thr Ser Glu Thr Lys Glu Phe Ser Asp Arg Glu Asp Ser 210 215 220	732
ttt tac tat aat cga ttt gat cat ttt aaa gat aga gta tta gta cct Phe Tyr Tyr Asn Arg Phe Asp His Phe Lys Asp Arg Val Leu Val Pro 225 230 235	780
ctc gca tat ata aaa ttt gat gaa tat ctt gaa gaa ctt cat gca gaa Leu Ala Tyr Ile Lys Phe Asp Glu Tyr Leu Glu Leu His Ala Glu 240 245 250 255	828
cgt cag aca tta aat aaa gac tta aac aaa gct cta aaa gat att gaa Arg Gln Thr Leu Asn Lys Asp Leu Asn Lys Ala Leu Lys Asp Ile Glu 260 265 270	876
aaa cga cca gat aac aaa aaa gca caa aat aaa aaa ata aat tta gaa Lys Arg Pro Asp Asn Lys Lys Ala Gln Asn Lys Lys Ile Asn Leu Glu 275 280 285	924
cag caa tta aaa gca aat gag caa aaa att gat gaa gca aca caa ctt Gln Gln Leu Lys Ala Asn Glu Gln Lys Ile Asp Glu Ala Thr Gln Leu 290 295 300	972
caa tta gaa cat ggt aac gaa tta cca ata tct gct gga ttc ttc ttt	1020

Gln Leu Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe			
305	310	315	
att aat cca ttt gaa gtt gta tat tat gca ggt gga acg tca aat aaa			1068
Ile Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys			
320	325	330	335
tat aga cac ttc gct gga agt tat gca gtt caa tgg act atg att aat			1116
Tyr Arg His Phe Ala Gly Ser Tyr Ala Val Gln Trp Thr Met Ile Asn			
340	345	350	
tat gca att gat cat ggc att gac cgt tat aat ttt tat ggg att agt			1164
Tyr Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser			
355	360	365	
ggt cat ttt aca gat gat gct gaa gat gca ggt gtt gta aaa ttt aaa			1212
Gly His Phe Thr Asp Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys			
370	375	380	
aaa gga ttt aat gca gat gta att gaa tat gtt ggt gat ttc gtt aaa			1260
Lys Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys			
385	390	395	
cct ata aat aaa cca atg tat tca cta tat aca aca ctt aaa aaa att			1308
Pro Ile Asn Lys Pro Met Tyr Ser Leu Tyr Thr Thr Leu Lys Lys Ile			
400	405	410	415
aaa aag aga ttgaatTAAG agggGAATAG tgagaa			1343
Lys Lys Arg			

<210> 53
 <211> 418
 <212> PRT
 <213> Staphylococcus hominis femA

 <400> 53

Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asp Phe Thr Glu			
1	5	10	15

Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu Leu			
20	25	30	

Lys Val Ala Glu Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn Lys			
35	40	45	

Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val Met			
50	55	60	

Lys Ile Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr			
65	70	75	80

Glu Asn Lys Glu Leu Val His Phe Phe Asn Glu Leu Ser Lys Tyr
85 90 95

Leu Lys Gln Gln His Cys Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro
100 105 110

Tyr Gln Tyr Arg Asn His Asp Gly Asp Ile Thr Gly Asn Ala Gly Asn
115 120 125

Asp Trp Phe Phe Asp Lys Met Lys Gln Leu Gly Tyr Gln His Glu Gly
130 135 140

Phe Thr Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser Val
145 150 155 160

Leu Asn Leu Lys Asp Lys Thr Ala Lys Asp Val Leu Asn Gly Met Asp
165 170 175

Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
180 185 190

Val Arg Phe Leu Thr Lys Glu Glu Leu Pro Ile Phe Arg Ser Phe Met
195 200 205

Glu Asp Thr Ser Glu Thr Lys Glu Phe Ser Asp Arg Glu Asp Ser Phe
210 215 220

Tyr Tyr Asn Arg Phe Asp His Phe Lys Asp Arg Val Leu Val Pro Leu
225 230 235 240

Ala Tyr Ile Lys Phe Asp Glu Tyr Leu Glu Glu Leu His Ala Glu Arg
245 250 255

Gln Thr Leu Asn Lys Asp Leu Asn Lys Ala Leu Lys Asp Ile Glu Lys
260 265 270

Arg Pro Asp Asn Lys Ala Gln Asn Lys Lys Ile Asn Leu Glu Gln
275 280 285

Gln Leu Lys Ala Asn Glu Gln Lys Ile Asp Glu Ala Thr Gln Leu Gln
290 295 300

Leu Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe Ile
305 310 315 320

Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys Tyr
325 330 335

Arg His Phe Ala Gly Ser Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr
340 345 350

Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
355 360 365

His Phe Thr Asp Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys Lys
370 375 380

Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys Pro
385 390 395 400

Ile Asn Lys Pro Met Tyr Ser Leu Tyr Thr Thr Leu Lys Lys Ile Lys
405 410 415

Lys Arg

<210> 54
<211> 1371
<212> DNA
<213> *Staphylococcus saprophyticus* femA

<220>
<221> CDS
<222> (64)..(1326)

<400> 54
acttgttag attagaatta aactcgaaaa tagaactata gataaatagg agtatataaa 60
aaa atg aaa ttt acg aat tta act gca aaa gag ttc ggt gca ttt acg 108
Met Lys Phe Thr Asn Leu Thr Ala Lys Glu Phe Gly Ala Phe Thr
1 5 10 15

gat aaa atg ccg aat agt cat ttt acg caa atg gtt gga aat tat gaa 156
Asp Lys Met Pro Asn Ser His Phe Thr Gln Met Val Gly Asn Tyr Glu
20 25 30

ttg aaa att gca gaa agt aca gaa aca cac cta gta ggt att aag aat 204
Leu Lys Ile Ala Glu Ser Thr Glu Thr His Leu Val Gly Ile Lys Asn
35 40 45

aat gat aat gaa gta att gca gca tgt tta ctt aca gct gtt cct gtt	252
Asn Asp Asn Glu Val Ile Ala Ala Cys Leu Leu Thr Ala Val Pro Val	
50 55 60	
atg aaa ttc ttc aag tat ttt tat tcc aat aga ggt cca gtc ata gat	300
Met Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp	
65 70 75	
ttt gaa aat aaa gaa ctc gta cat tac ttc ttt aac gaa tta gca aaa	348
Phe Glu Asn Lys Glu Leu Val His Tyr Phe Phe Asn Glu Leu Ala Lys	
80 85 90 95	
tat gta aaa aaa cat aat gcc tta tat tta cga gta gat cct tat ctt	396
Tyr Val Lys Lys His Asn Ala Leu Tyr Leu Arg Val Asp Pro Tyr Leu	
100 105 110	
gct tat caa tat cgt aat cat gat ggt gaa gta tta gca aat gcg ggt	444
Ala Tyr Gln Tyr Arg Asn His Asp Gly Glu Val Leu Ala Asn Ala Gly	
115 120 125	
cac gat tgg att ttt gat aaa atg aaa caa ctc ggt tat aag cat gaa	492
His Asp Trp Ile Phe Asp Lys Met Lys Gln Leu Gly Tyr Lys His Glu	
130 135 140	
ggt ttt tta act ggc ttt gac cca ata ctt caa ata aga ttc cat tct	540
Gly Phe Leu Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser	
145 150 155	
gtt tta gat tta gct gga aaa act gct aaa gac gta ctt aat ggt atg	588
Val Leu Asp Leu Ala Gly Lys Thr Ala Lys Asp Val Leu Asn Gly Met	
160 165 170 175	
gat agt tta cgt aaa cga aat act aaa aaa gta cag aaa aat ggt gtg	636
Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val	
180 185 190	
aaa gta aga ttt tta ggt gaa gat gag ttg cca ata ttc cgc tca ttc	684
Lys Val Arg Phe Leu Gly Glu Asp Glu Leu Pro Ile Phe Arg Ser Phe	
195 200 205	
atg gaa gat act tct gaa aca aag gat ttt gac gat aga gat gac gat	732
Met Glu Asp Thr Ser Glu Thr Lys Asp Phe Asp Asp Arg Asp Asp Asp	
210 215 220	
ttt tat tat aat agg tta aga tat tat aaa gat cgt gtg ctt gtc cca	780
Phe Tyr Tyr Asn Arg Leu Arg Tyr Tyr Lys Asp Arg Val Leu Val Pro	
225 230 235	
tta gct tat atg gat ttt gat gaa tat ata aca gaa tta aag gct gaa	828
Leu Ala Tyr Met Asp Phe Asp Glu Tyr Ile Thr Glu Leu Lys Ala Glu	
240 245 250 255	
cgc gaa gta tta agt aaa gat ata aat aaa gca gtt aag gat ata gaa	876
Arg Glu Val Leu Ser Lys Asp Ile Asn Lys Ala Val Lys Asp Ile Glu	
260 265 270	
aaa aga cca gaa aat aaa aaa gcg tat aat aaa aaa gaa aat tta gaa	924

Lys Arg Pro Glu Asn Lys Lys Ala Tyr Asn Lys Lys Glu Asn Leu Glu	275	280	285		
caa caa ctg att gca aac caa caa aaa ata gat gaa gcc act gcg tta	290	295	300	972	
Gln Gln Leu Ile Ala Asn Gln Gln Lys Ile Asp Glu Ala Thr Ala Leu					
caa gag aag cat ggt aac gaa tta ccg att tct gca gct tac ttt att	305	310	315	1020	
Gln Glu Lys His Gly Asn Glu Leu Pro Ile Ser Ala Ala Tyr Phe Ile					
att aat cct tat gaa gtc gtt tac tat gca ggt ggt aca tct aat gaa	320	325	330	335	1068
Ile Asn Pro Tyr Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Glu					
ttt aga cat ttt gct ggt agt tat gca ata caa tgg aag atg att aat	340	345	350	1116	
Phe Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Lys Met Ile Asn					
tat gct ata gat cat aat ata gat aga tat aat ttt tat ggt att agt	355	360	365	1164	
Tyr Ala Ile Asp His Asn Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser					
ggt cat ttt act gaa gat gca gaa gat gca ggt gtt gtt aaa ttt aaa	370	375	380	1212	
Gly His Phe Thr Glu Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys					
aaa ggt ttt aat gca gat gta gta gaa tat gtt ggt gat ttt att aaa	385	390	395	1260	
Lys Gly Phe Asn Ala Asp Val Val Glu Tyr Val Gly Asp Phe Ile Lys					
ccg att aat aag cca atg tac aaa att tat acg aca ttg aaa aaa att	400	405	410	1308	
Pro Ile Asn Lys Pro Met Tyr Lys Ile Tyr Thr Thr Leu Lys Lys Ile					
aag gat aaa aag aaa taa acataaaatag aaggaaacta agctagaatg	420			1356	
Lys Asp Lys Lys Lys					
aaatttacag aqutta				1371	

<210> 55
<211> 420
<212> PRT
<213> *Staphylococcus saprophyticus* femA

<400> 55

Met Lys Phe Thr Asn Leu Thr Ala Lys Glu Phe Gly Ala Phe Thr Asp
1 5 10 15

Lys Met Pro Asn Ser His Phe Thr Gln Met Val Gly Asn Tyr Glu Leu
20 25 30

Lys Ile Ala Glu Ser Thr Glu Thr His Leu Val Gly Ile Lys Asn Asn
35 40 45

Asp Asn Glu Val Ile Ala Ala Cys Leu Leu Thr Ala Val Pro Val Met
50 55 60

Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Phe
65 70 75 80

Glu Asn Lys Glu Leu Val His Tyr Phe Phe Asn Glu Leu Ala Lys Tyr
85 90 95

Val Lys Lys His Asn Ala Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala
100 105 110

Tyr Gln Tyr Arg Asn His Asp Gly Glu Val Leu Ala Asn Ala Gly His
115 120 125

Asp Trp Ile Phe Asp Lys Met Lys Gln Leu Gly Tyr Lys His Glu Gly
130 135 140

Phe Leu Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser Val
145 150 155 160

Leu Asp Leu Ala Gly Lys Thr Ala Lys Asp Val Leu Asn Gly Met Asp
165 170 175

Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
180 185 190

Val Arg Phe Leu Gly Glu Asp Glu Leu Pro Ile Phe Arg Ser Phe Met
195 200 205

Glu Asp Thr Ser Glu Thr Lys Asp Phe Asp Asp Arg Asp Asp Phe
210 215 220

Tyr Tyr Asn Arg Leu Arg Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu
225 230 235 240

Ala Tyr Met Asp Phe Asp Glu Tyr Ile Thr Glu Leu Lys Ala Glu Arg
245 250 255

Glu Val Leu Ser Lys Asp Ile Asn Lys Ala Val Lys Asp Ile Glu Lys

260

265

270

Arg Pro Glu Asn Lys Lys Ala Tyr Asn Lys Lys Glu Asn Leu Glu Gln
275 280 285

Gln Leu Ile Ala Asn Gln Gln Lys Ile Asp Glu Ala Thr Ala Leu Gln
290 295 300

Glu Lys His Gly Asn Glu Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile
305 310 315 320

Asn Pro Tyr Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe
325 330 335

Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr
340 345 350

Ala Ile Asp His Asn Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
355 360 365

His Phe Thr Glu Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys Lys
370 375 380

Gly Phe Asn Ala Asp Val Val Glu Tyr Val Gly Asp Phe Ile Lys Pro
385 390 395 400

Ile Asn Lys Pro Met Tyr Lys Ile Tyr Thr Thr Leu Lys Lys Ile Lys
405 410 415

Asp Lys Lys Lys
420

<210> 56
<211> 18
<212> DNA
<213> artificial sequence
<223> femX1 oligonucleotide

<220>
<221> misc_feature
<222>
<223> M= A or C

<400> 56
ttcmaatcgc ggtccagt

18

<210> 57
<211> 23
<212> DNA
<213> artificial sequence
<223> femX2 oligonucleotide

<400> 57
caagaacatg gcaacgaatt acc

23

<210> 58
<211> 23
<212> DNA
<213> artificial sequence
<223> femX3 oligonucleotide

<400> 58
tggtaattc gttgccatgt tct

23

<210> 59
<211> 21
<212> DNA
<213> artificial sequence
<223> femX4 oligonucleotide

<400> 59
ccaagcatct tcagcatctt c

21

<210> 60
<211> 29
<212> DNA
<213> artificial sequence
<223> femX5 oligonucleotide

<400> 60
ttcttaact gttaactctg taaatttca

29

<210> 61
<211> 26
<212> DNA
<213> artificial sequence
<223> femX6 oligonucleotide

<400> 61
acatatttac ttaattcggtt aaagaa

26

<210> 62
<211> 27
<212> DNA
<213> artificial sequence
<223> femX7 oligonucleotide

<400> 62
cagaaaaatg gtgttaaagt aagattt

27

<210> 63
<211> 27
<212> DNA
<213> artificial sequence
<223> femX8 oligonucleotide

<400> 63
aagaaaatctt actttcacac cattttt

27

<210> 64
<211> 18
<212> DNA
<213> artificial sequence
<223> femX9 oligonucleotide

<400> 64
aactcgaaaa tagaacta

18